

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw modeL

Run on:

September 30, 2003, 16:35:33 ; Search time 414.636 Seconds

(without alignments)
12661.132 Million cell updates/sec

Title: US-09-856-681-3
Perfect score: 216
Sequence: 1 ccgcgcgcgcgcgcgcagag.....agccaaatgtatgcgtgtaca 216

Scoring table: IDENTITY_NUC , Gapext: 1.0

Searched: 22781392 seqs; 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:
2: em_estbm:
3: em_estin:
4: em_estml:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_htc:
9: gb_est1:
10: gb_est2:
11: gb_htc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estinr:
16: em_eston:
17: em_gss_bum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rnd:
26: em_gss_phg:
27: gb_gss1:
28: gb_gss2:
29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	216	100.0	495 12	BM855120 BM855120 K-EST0137
2	216	100.0	496 9	AVT04776 AVT04776
3	216	100.0	815 13	BU750015 AGENCOURT
4	100.0	862 13	BQ723018 AGENCOURT	

ALIGNMENTS

RESULT 1				
BM855120	BM855120			
DEFINITION	K-EST0137999 S22SNUL6n1	495 bp	mRNA	linear EST 06-MAR-2002
LOCUS				
ACCESSION	BM855120	5', mRNA sequence.		
VERSION	BM855120.1	GI:19211519		
KEYWORDS				
EST.				
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 495)			
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and			
TITLE	21C Frontier Korean EST Project 2001			
JOURNAL	Unpublished			
COMMENT	Contact: Kim YS			
	Genome Research Center			
	Korea Research Institute of Bioscience & Biotechnology			
	52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea			
	Tel: +82-42-860-4470			
	Fax: +82-42-860-4409			
	Email: yongsung@mail.kribb.re.kr			
	Plate: 150 row; D column: 07			
	High quality sequence step: 495.			

FEATURES
source
location/Qualifiers

1. . 495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Taxon:9606"
/clone="S22SNU16n1-150-D07"
/sex="P"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/lab_host="DHL08"
/clone_lib="S22SNU16n1"

/note="origin: stomach; vector: pT7f3-Pac; Site_1: EcoRI; Site_2:
/cell_line="SNU-16"
/lab_host="DHL08"
/clone_lib="ADB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
/XbaI"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
/XbaI";

Site_2: Note: The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996). Genome Research 9(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB), SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990). Cancer Res 50: 2773-2780.

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 216; DB 12; length 495;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 CCCCGCGCCGCCGAGGGGACTCAGCTCAGGACAGCTCCAGCATCAGC 60
99 CAGGCCGAGCTGTCTCAGGCCAACGCTAACACTACTGAGAAGGRCG 158
Db
39 CGCGCGCCGCCGCCAGGGGACTCAGCTCAGGACAGCTCCAGCATCAGC 98

QY
61 CAGGCCGAGCTGTCTCAGGCCAACGCTAACACTACTGAGAAGGRCG 120
159 GGGCTGAGCGTAGCCCTCGCTAAAGCGGGAGGTACCCCCAACACCCACCTTGCTCCC 180
Db
181 CTTTCCACATCCATGAAGGCCAATGATGCGTGTACA 216

QY
219 CTTTCCACATCCATGAAGGCCAATGATGCGTGTACA 254

RESULT 2
AV04776 AV704776 AV704776 ADB Homo sapiens 496 bp mRNA linear EST 09-OCT-2000
DEFINITION AV704776 ADB Homo sapiens cDNA clone ADJBTC04 5', mRNA sequence.
VERSION AV704776.1 GI:10722088
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS NIH-MCC
TITLE NIH-MCC
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
DNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LUCM282 row: b column: 18
High quality sequence stop: 700.
Location/Qualifiers
1. . 815
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Taxon:9606"
/clone="IMAGE:659870"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DHL08 (phage-resistant)"
/clone_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
XbaI; cDNA made by oligo-dT priming, Directionally cloned
into BcoRI/XbaI sites using the following 5' adaptor:

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Taxon:9606"
/clone="ADB:TC04"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLN"
/clone_lib="ADB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
/XbaI";

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
/XbaI";

BASE COUNT

107 a 178 c 131 g 80 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 216; DB 9; Length 496;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 CCCCGCGCCGCCGAGGGGACTCAGCTCAGGACAGCTCCAGGCTCAGC 60
Db
61 CAGGCCGAGCTGTCTCAGGCCAACGCTAACACTACTGAGAAGGRCG 120
241 CAGGCCGAGCTGTCTCAGGCCAACGCTAACACTACTGAGAAGGRCG 300

QY
121 GGGCTGAGCGTAGCCCTCGCTAAAGCGGGAGGTACCCCCAACACCCACCTTGCTCCC 180
301 GGCTGAAGCTGTAAGCCCTCGCTAAAGCGGGAGGTACCCCCAACACCCACCTTGCTCCC 360

QY
181 CTTTCCACATCCATGAAGGCCAATGATGCGTGTACA 216

Db
361 CTTTCCACATCCATGAAGGCCAATGATGCGTGTACA 396

RESULT 3
BU850016 BU850016

LOCUS BU850016
DEFINITION AGENCOURT_10431272_NIH_MSC_109 Homo sapiens cDNA clone IMAGE:6598770 5', mRNA sequence.

ACCESSION BU850016
VERSION BU850016.1 GI:24034979

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MCC
AUTHORS NIH-MCC
TITLE NIH-MCC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: ATCC
DNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LUCM282 row: b column: 18
High quality sequence stop: 700.
Location/Qualifiers
1. . 815
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="Taxon:9606"
/clone="IMAGE:659870"
/tissue_type="teratocarcinoma, cell line"
/lab_host="DHL08 (phage-resistant)"
/clone_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
XbaI; cDNA made by oligo-dT priming, Directionally cloned
into BcoRI/XbaI sites using the following 5' adaptor:

FEATURES
source
comment
contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujiong Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P.R. China
Tel: 86-21-50801922
Fax: 86-21-50801922
Email: hanzg@cgcc.sh.cn

This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. . 496

GCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library."

BASE COUNT 236 a 27_ c 172 g 136 t
ORIGIN

Query Match 100.0%; Score 216; DB 13; Length 815;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGCGGCCGCCGCCAGAGGGACTCCATCAGGTCACAGCTCCAGCCATCTGGC 60
95 CC CG CG CG CG CC CG CA CG GT GC AT CG TC AG GT GC AC AG CT CC AG CC AT CT GG C 155
Db 61 CAGGGCTGACTGCTCAGGGTGCACATCAGGTGCACAGCTCCAGCCATCTGGC 120
155 CAGCCGCGACTGCTGCTGAGGCACCCGCTCACGCTACACTCACTGACAGGTG 215
QY 121 GG GT GA AG GT TA CG CC C H OG CH RA AS CG G A G T A C C C C C A A C C A T C C T T G C C C 180
216 GG GT GA AG GT TA CG CC C H OG CH RA AS CG G A G T A C C C C C A A C C A V C C T T G C I C C 275
Db 329 CAGCCGCGACTGCTGCTGAGGCACCCGCTCACGCTACACTCACTGACAGGTG 388
QY 121 GG GT GA AG GT TA CG CC C H OG CH RA AS CG G A G T A C C C C C A A C C A T C C T T G C C C 180
389 GG GT GA AG GT TA CG CC C H OG CH RA AS CG G A G T A C C C C C A A C C A V C C T T G C T C C 448
QY 181 CTTTCCACATCCATGAAGCCAAATGATGAGTGGTGTACA 216
276 CTTTCCACATCCATGAAGCCAAATGATGAGTGGTGTACA 311

RESULT 4

LOCUS B0723018 862 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT 8099701 Lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6190272 5', mRNA sequence.
ACCESSION B072301
VERSION B0723018.1 GI:21861915
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 862)
AUTHORS NIH-MGC
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgbps-1@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
Plate: L1AM1358B row: n column: 01
High quality sequence stop: 592.
FEATURES source

location/Qualifiers
1. .862
/organism="Homo sapiens"
/mol_type="mRNA"
/ab_xref="taxon:9606"
/clone="IMAGE:6190272"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult; 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic-trunk"
/note="vector: PCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming; directionally cloned into EcoRI/XbaI sites using the following 5'-TCGACCGCGTCGCG-3', and 5'-GACGATGCTAGTCGAGCCGCGCT(15)-3' size selected >1 kb for average insert length 1.9 kb. This is a primary

BASE COUNT 208 a 307 c 207 g 140 t
ORIGIN

Query Match 100.0%; Score 216; DB 13; Length 862;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGCGGCCGCCGCCAGAGGGACTCCATCAGGTCACAGCTCCAGCCATCTGGC 60
269 CC CG CG CG CC CG CAG AG GT G ACT C AT CG GT GC AC AG CT CC AG CC AT CT GG C 328
Db 61 CAGGGCTGACTGCTCAGGGTGCACATCAGGTGCACAGCTCCAGCCATCTGGC 120
329 CAGCCGCGACTGCTGCTGAGGCACCCGCTCACGCTACACTCACTGACAGGTG 388
QY 121 GG GT GA AG GT TA CG CC C H OG CH RA AS CG G A G T A C C C C C A A C C A T C C T T G C C C 180
389 GG GT GA AG GT TA CG CC C H OG CH RA AS CG G A G T A C C C C C A A C C A V C C T T G C T C C 448
QY 181 CTTTCCACATCCATGAAGCCAAATGATGAGTGGTGTACA 216
Db 449 CTTTCCACATCCATGAAGCCAAATGATGAGTGGTGTACA 484

RESULT 5

LOCUS BB98612 928 bp mRNA linear EST 29-SEP-2000
DEFINITION 601681550F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951685 5', mRNA sequence.
ACCESSION BB98612
VERSION BB98612.1 GI:10365266
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 928)
AUTHORS NIH-MGC
TITLE NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgbps-1@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.lnl.gov
Plate: L1CH820 row: c column: 14
High quality sequence stop: 794.
FEATURES source

location/Qualifiers
1. .928
/organism="Homo sapiens"
/mol_type="mRNA"
/ab_xref="taxon:9606"
/clone="IMAGE:391685"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/note="Organ: ovary; Vector: pORT7; Site_1: XbaI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5'-TCGACCGCGTCGCG-3', and 5'-GACGATGCTAGTCGAGCCGCGCT(15)-3' size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 245 a 314 c 215 g 154 t
ORIGIN

library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

BASE COUNT 111 a 167 c 103 g 77 t 4 Others
ORIGIN

Query Match 98.1%; Score 212; DB 14; Length 462;
Best Local Similarity 98.1%; Pred. No. 1.1e-46; Indels 0; Gaps 0;
Matches 212; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CCGCCGCCGCCGCCAGGGTGACTCCATCCAGGTGCAAGCTCCAGGCATCTGGC 60
Db 238 CCGCCGCCGCCGCCAGGGTGACTCCATCCAGGTGCAAGCTCCAGGCATCTGGC 297
QY 61 CAGGGCGGAGCTGCTGAGGGAGGCCAGCCTAACCCCTACACTACTGAGGTGCG 120
Db 298 CAGGCCGAGCTGCTGAGGGAGGCCAGCCTAACCCCTACACTACTGAGGTGCG 357
QY 121 GGCTGTGAGCTGAGGGAGGCCAGCCTAACCCCTACACTACTGAGGTGCG 180
Db 358 GGCTGTGAGCTGAGGGAGGCCAGCCTAACCCCTACACTACTGAGGTGCG 417
QY 181 CTTCGACATCCATGAAGCCCATGAGGGTGTACA 216
Db 418 CTTCGACATCCATGAAGCCCATGAGGGTGTACA 453

RESULT 10

N46020 LOCUS N46020 410 bp mRNA linear EST 14-FEB-1996
DEFINITION YY35405.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:2732005, mRNA sequence.

ACCESSION N46020

VERSION N46020.1

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Hillier,L., Clark,N., Dubuke,T., Elliston,K., Hawkins,M., Holman

TITLE

Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston

JOURNAL

, R., Williamson,A., Wohldmann,P. and Wilson,R.

COMMENT

The WashU-Merck EST Project

Unpublished

Contact:

Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LINCS; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: T7

High quality sequence stop: 329.

LOCATION/QUALIFIERS

1. 410

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:3882842"

/db_xref="taxon:9606"

/clone="IMAGE:273200"

/tissue_type="melanocyte"

/lab_host="DHIOB (ampicillin resistant)"

/clone="Soares melanocyte 2NbHM"

/note="Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

TETTACAACTGAGGGAGCGGGCAGTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

BASE COUNT 99 a 143 c 101 g 62 t 5 others
ORIGIN

Query Match 94.3%; Score 203.6; DB 14; Length 410;
Best Local Similarity 94.3%; Pred. No. 1.9e-44; Indels 0; Gaps 0;
Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CCGCCGCCAGGGGGTGACTCATCCAGGTGACAGCTCCAGCCATCTGGCC 66
Db 78 CCGCCGCCAGGGGGTGACTCATCCAGGTGACAGCTCCAGCCATCTGGCC 137

QY 67 GTRACTGCTGGGGACCCCACTCAGCCCTACACTCTAGACAGGTGGGGC 126

Db 138 GTRACTGCTGGGGACCCCACTCAGCCCTACACTCTAGACAGGTGGGGC 197

QY 127 AASGTTAGCCCTCGTAAGCGGGACCTACCCCAACCATCTTGTCTCCCTTGC 186

Db 198 AACCTGAGCCCGCTTAAGCGGGACCTACCCCAACCATCTTGTCTCCCTTGC 257

Db 258 ACATCCATGAAGCCAATGATGTTGTACA 287

RESULT 11

CB577257 LOCUS CB577257 632 bp mRNA linear EST 03-APR-2003
DEFINITION AMGNNUC:CDRG1-00015-G10-A cdrg1 (10898) Rattus norvegicus cDNA
IMAGE:cdrg1-00015-g10 5, mRNA sequence.

ACCESSION CB577257

VERSION CB577257.1

KEYWORDS EST.

SOURCE

ORGANISM

Rattus norvegicus (Norway rat)

REFERENCE

Rattus; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

AUTHORS

1 (bases 1 to 632)

TITLE

Amgen EST Program.

JOURNAL

Amgen Rat EST Program

COMMENT

Unpublished

Contact: Dan Fitzpatrick

Amgen, Inc

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00015

row: g column: 10.

FEATURES

source

1. 632

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="cdrg1-00015-g10"

/tissue_type="Chung Model ipsilate"

/clone.lib="cdrg1 (10898)"

/note="psORT1; Chung Model Rat DRG Left L5/L6"

BASE COUNT 155 a 213 c 151 g 113 t
ORIGIN

Query Match 89.6%; Score 193.6; DB 14; Length 632;
Best Local Similarity 89.5%; Pred. No. 1.1e-41; Indels 14; Gaps 0;
Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 CCGCCGCCAGGGGGTGACTCATCCAGGTGACAGCTCCAGCCATCTGGC 60
Db 20 CCACCCGCCGCCAGGGGGTGACTCATCCAGGTGACAGCTCCAGCCATCTGGC 79

QY 61 CAGGCGTGTACTCTGGAGCCACCCGACCTCACCGCTACACTGAAAGGGC 120
 Db 80 CAGGCCGTTGACTGCTTGAGGCAGCCACGCTCAATGOTACACTACTGAGAGGRCG 139
 QY 121 GGCTGTAAGCTGAGCCCTCGCTAAAGCGGGACTAACCCCAACCATCCTTGCC 180
 Db 140 GGCTGTAAGCTGAGCCCTCGCTAAAGCGGGACTAACCCCAACCATCCTTGCC 199
 Qy 181 CTTCACATCCATGAAGCCATGTGAGTGTACCCAAACTCTCTGTCAC 216
 Db 200 CTTCACATCCATGAAGCCATGTGAGTGTACCA 235

RESULT 12
 CB46380 Locus CB246380 711 bp mRNA linear EST 12-FEB-2003
 DEFINITION UT-M_F10-cdw-i-10-0-UT.r1 NIH_BMAP_F10 Mus musculus cDNA clone
 IMAGE: 6835379 5', mRNA sequence.
 ACCESSION CB246380
 VERSION CB246380.1 GI:28368024
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 711)
 AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgrabs@final.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIN at: http://image.lnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP).
 The following repetitive elements were found in this cDNA:
 sequence: 563-605, >(CA)SimpleName_repeat
 Seq primer: PYX-5
 Location/Qualifiers
 1..711
 FEATURES Source
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10116"
 /clone="mrpe3-00075-d4"
 /tissue="whole brain"
 /clone="IMAGE: 6835379"
 /dev_stage="embryo 12.5dpc"
 /clone="Lib=NIH_BMAP_F10"
 /lab_host="NIH_BMAP_F10"
 /note="Organ: Brain; Vector: PYX-5; Asc: Site_1: EcoR I; Site_2: Not I; The library was constructed according to the method of Bonaldo, Lennon and Soares, Genome Research, 6:71-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adapter, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCAGAC. This library was created for the University Iowa Brain Anatomy Project (BMAP); Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator." 125 t 1 others
 BASE COUNT ORIGIN
 189 a 255 c 141 g 125 t 1 others
 Query Match 89.6%; Score 193.6; DB 14; Length 2411;
 Best Local Similarity 93.5%; Pred. No. 1.1e-41; Indels 0; Gaps 0;
 Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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 Db 1340 CAACCCCGCCCGAGGGTCACTCATCCAGGTGACGCGCTAACGCGCTATCCAGGTCACGCTCCAGCATTCTGGC 1399
 QY 61 CAGGCGTGTACTCTGGAGCCACCCGACCTCACCGCTACACTGAAAGGGC 120
 Db 1400 CAGGCCGTTGACTGCTTGAGGCAGCCAGCTCAATGCTTACACTGAGAGGRCG 1459
 QY 121 GGCTGTAAGCTGAGCCCTCGCTAAAGCGGGACTAACCCCAACCATCCTTGCC 180
 Db 1460 GGCTGTAAGCTGAGCCCTCGCTAAAGCGGGACTAACCCCAACCATCCTTGCC 199
 QY 181 CTTCACATCCATGAAGCCATGTGAGTGTACCCAACTCTGTCAC 216
 Db 1520 CTTCACATCCATGAAGCCATGTGAGTGTACCA 235

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Om nucleic - nucleic search, using sw model

Run on:

September 30, 2003, 16:34:33 ; Search time 773.266 Seconds

{without alignments}

11427.482 Million cell updates/sec

Title: US-09-856-681-3

Sequence: 1 ccggccgcgcgcgcagag.....agcccaatgtatgtgtaca 216

Perfect score: 216

Scoring table: IDENTITY.NUC

Gapop 10.0 , Gapext 1.0

Searched: 288711 seqs, 2045481386 residues

Total number of hits satisfying chosen Parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_hiq:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mil:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

RESULT 1
AX026743 LOCUS AX026743
DEFINITION Sequence 3 from Patent WO0031252.
ACCESSION AX026743
VERSION AX026743.1 GI:10187888
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bilateria; Animalia; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

Pred. No. is the number of results predicted by chance to have a

JOURNAL	use as a potential drug target	source	1. . 2123
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source	/db_xref="GI:10187889"	/db_xref="taxon:9606"	
CDS	/translation="PPPARQVDSIQVHSQSPOQAVTWSRQPSLNAYNSLIRSGIKRTPSLKPDPPKSPFAPLSMVKPNDAT"	BASE COUNT	45 a 85 c 51 g 35 t
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BASE COUNT	550 a 664 c 528 g 381 t	ORIGIN	Query Match 100.0%; Score 216; DB 6; Length 2123; Best Local Similarity 100.0%; Pred. No. 8.4e-42; Matches 216; Conservative 0; Mismatches 0; Indels 0; gaps 0; Qy 1 CCGCCGCCGCCCCGGAGAGGGTGGACTCCATCCAGGTGGACAGCTCCAGCCATCTGGC 60 Db 1552 GGGCTTGAGGGTACGCTCTCTAAAGCCGAGTACCCCTAACCTCTGGC 1611 Db 1612 CTTTCCACATCATGAGGCCATGTCGGTACA 1647
RESULT 2	BD155987	RESULT 3	AK027439
DEFINITION	LOCUS BD155987	DEFINITION	AK027439
ACCESSION BD155987	DEFINITION	ACCESSION	AK027439
VERSION BD155987.1	LOCUS	VERSION	AK027439.1
KEYWORDS	REFERENCE	KEYWORD	GI:14042113
SOURCE	AUTHORS	SOURCE	Oligo capping (full insert sequence).
ORGANISM	REFERENCE	ORGANISM	Homo sapiens (human), Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	AUTHORS	REFERENCE	
Bivalvia; Bivalvia; Mollusca; Gastropoda; Euthyneura; Neodermata; Malacostraca; Decapoda; Caridea; Palaemonidae; Caridina;	1. Isogai,T., Ota,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.	AUTHORS	
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. (bases 1 to 2123)	1. Isogai,T., Ota,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.	TITLE	
COMMENT	JOURNAL	TITLE	
OS Homo sapiens (human)	COMMENT	JOURNAL	
PI TOSHIRO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI	COMMENT	GENOMICS LABORATORY; 1532-3 Yana-Kisarazu, Chiba 291-0812, Japan (E-mail: genomics@nrl.co.jp; Tel: +81-438-52-3975, Fax: +81-438-52-3986)	
PC C12N1/5-09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5 / db_xref="taxon:9606"	FEATURES	COMMENT	
PC C12B21/02, C12Q1/68//C12B21/08, G06F17/30, C12N5/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof	source	Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute, (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.	
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PI JPN 2002191363-A/10830	Location/Qualifiers	1. . 2123	
PD 09-JUL-2002	Location/Qualifiers	/organism="Homo sapiens"	
PF 28-JUL-2000 JP 2000280990	Location/Qualifiers	/mol_type="mRNA"	
PI SATTO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI	Location/Qualifiers	/db_xref="taxon:9606"	
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FEATURES	Location/Qualifiers		

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Best Local Similarity	100.0%	Pred. No. 8. 3e 42;
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DB	1608	CGGCCGCCGCCGCCGCCAGGGTGGACTCCATCAGGTGACAGCCATCTGGC 1667
QY	61	CAGGCCGTACTGCTGAGGGAGCCAGCCCTAACGCTACAGCTACTGAGTCG 120
DB	1668	CAGGCCGTGACTGTCTGAGGCCAGCCAGCCATCTGGC 1727
QY	121	GAGCTGAGCGTAGCCCTCGTAAGCCGAGTACCCCGAACCATCTTGCTCC 180
DB	1728	GGCTGAGCGTAGCCCTCGTAAGCCGAGTACCCCGAACCATCTTGCTCC 1787
QY	181	CTTCCACATCCATGAGGCCCATATGATGCCATCA 216
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DEFINITION		Primer for synthesizing full-length cDNA and use thereof.
ACCESSION		BD159853
VERSION		1.0
KEYWORDS		1728
SOURCE		181
ORGANISM		CTTCCACATCCATGAGGCCCATATGAGCTG 1830
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.	
TITLE	JOURNAL	
Patent: JP 2002191363-A 14696 09-JUL-2002; HELIX RESEARCH INSTITUTE		
COMMENT		
OS	Homo sapiens (human)	
PI	JP 2002191363-A/14696	
PD	09-JUL-2002	
PF	28-JUL-2000	
PI	TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SATO, JUNICHI YAMAMOTO, SHIZUKO ISHTI, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI	
PC	C12M15/03, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00	
Primer for synthesizing full-length cDNA and use thereof RH	CC	
Location/Qualifiers	Key	
FT	CDS	Location/Qualifiers (109). (1830).
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BASE COUNT	579 a	739 c
ORIGIN	579 a	577 g
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Best Local Similarity	100.0%	Pred. No. 8. 3e 42;
Matches	216;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	61	CAGGCCGTACTGCTGAGGGAGCCAGCCCTAACGCTACAGCTACTGAGTCG 120
DB	1675	CAGGCCGTACTGCTGAGGCCAGCCAGCCCTAACGCTACAGCTACTGAGTCG 1734
QY	121	GGGCTGAGCGTAGCCCTCGTAAGCCGAGTACCCCGAACCATCTTGCTCC 180
DB	1735	GGGCTGAGCGTAGCCCTCGTAAGCCGAGTACCCCGAACCATCTTGCTCC 1794
QY	181	CTTCCACATCCATGAGGCCCATATGAGCTG 216
DB	1795	CTTCCACATCCATGAGGCCCATATGAGCTG 1830
RESULT 9		
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DEFINITION		Homo sapiens cDNA FLJ14748 fis, clone NT2RP3002869, highly similar to <i>Mus musculus</i> semaphorin Vira mRNA.
ACCESSION		AK027654
VERSION		AK027654.1 GT:14042491
KEYWORDS		0190 capping; fis (full insert sequence).
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1	
AUTHORS	Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Hosoiri,T., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoi,T., Kaku,T., Kodaira,H., Kondo,H., Suewara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakami,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,T., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahariki,K., Masuho,I., Niromiya,K. and Iwayanagi,T.	
TITLE	JOURNAL	
Patent: JP 2002191363-A 14696 09-JUL-2002; HELIX RESEARCH INSTITUTE		
COMMENT		
OS	Homo sapiens (human)	
PI	JP 2002191363-A/14696	
PD	09-JUL-2002	
PF	28-JUL-2000	
PI	TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SATO, JUNICHI YAMAMOTO, SHIZUKO ISHTI, TOMOYASU SUGIYAMA, AI WAKAMATSU, KEIICHI NAGAI, TETSUJI OTSUKI	
PC	C12M15/03, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12P21/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00	
Primer for synthesizing full-length cDNA and use thereof RH	CC	
Location/Qualifiers	Key	
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109. .1833
/ncte="unnamed protein product"

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BASE COUNT
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Qy	Db	Qy	Db
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QY
181 CTTTCACATCCATGAAGCCAATGATCGCTGTACCA 216
|||||
1825 |||||
1830 |||||

DD 1/95 UTTTCAACATGAAAGCCAAATGATGCGTGAA 103U

RESOLN 10
BD159617
LOCUS

DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD159617
VERSION BD159617_1 GT:2785375
KEYWORDS JP 2002191363A/14460.
ORGANISM Homo sapiens (human)
NOTE: See also: 100-00000000000000000000000000000000

ORGANISME non sapientis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
PREFERENCE 1 (choose 100%).

KUROHIGUCHI,
AUTHORS
TITLE
I possest a CD player
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nakai,K., and Otsuka,T.
priher for synthesizing full-length cDNA and use thereof

COMMENT JOURNAL

PN JP 2002191363-A/14460
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIRO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO,
JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU
PT KENJI TSUTOMU OONUMA

FH KEIICHI NAGAI, EIJIUJI OISUKI
PC PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/9, C12N1/21, C12N5/10,
C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers

FEATURES	FT	CDS	Location/Qualifiers
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	216	714 g	637 t
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Best Local Similarity	100 %	Pred. No. Be-42;	
Matches	216;	Mismatches 0;	
Accession	Conservative	Indels 0;	
Version		Gaps 0;	
Keywords			
Organism			
RESULT 11			
Locus	AK027501	3041 bp	mRNA linear PR1 01-AUG-2002
Definition	Homo sapiens cDNA FLJ14595	fos, clone NT2RM4	002194, highly similar
Author	to Mus musculus semaphorin via mRNA.		
Accession	AK027501		
Version	AK027501.1	GI:1444222	
Keywords	oligo capping; fos (full insert sequence).		
Organism	Homo sapiens (human)		
Title	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
Reference	1		
Author	Isgai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Nagatsuma,M., Hosoi,T., Y., Kohara,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiuchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Niromiya,K. and Iwayanagi,T., Nakamura,Y., Nagai,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T., NEDO human cDNA sequencing project		
Journal	Unpublished		
Title	2 (bases 1 to 3041)		
Reference	Isgai,T. and Otsuki,T.		
Author	Direct Submission		
Journal	Submitted (10-MAY-2001) Takeo Isgai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@helix.co.jp, Tel: 81-438-52-3986)		
Comment	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5' - & 3' - end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.		
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BASE COUNT	804 a 886 c 714 g 637 t
ORIGIN	
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	Best Local Similarity 100.0%; Pred. No. 8e-42; Indels 0; Gaps 0;
	Matches 216; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
Qy	1 CGCCGCCGCCGCCAGAGGGTGACTCAATCCAGGTGACAGCTCCAGCCATCTGGC 60
Db	1968 CGCCGCCGCCGCCAGAGGGTGACTCAATCCAGGTGACAGCTCCAGCCATCTGGC 2025
Qy	61 CAGGCGTGAATGTCAGGAGCCAGCCATCAACGCTTACACTTGACAGGTG 120
Db	2026 CAGGCCTGACTGTCTGAGGCCAGCCATCAACGCTTACACTTGACAGGTG 2085
Qy	121 GGCGTGAAGCTACGCCCTCGTAAGCCGAGCTACCCCAACCATCTTGCTCC 180
Db	2086 GGCGTGAAGCTACGCCCTCGTAAGCCGAGCTACCCCAACCATCTTGCTCC 2145
Qy	181 CTTCACATCATGAGGCCAATGATGCGTGTACA 216
Db	2146 CTTCACATCATGAGGCCAATGATGCGTGTACA 2181
BASE COUNT	813 a 855 c 765 g 660 t
ORIGIN	
	Query Match 100.0%; Score 216; DB 6; Length 3093;
	Best Local Similarity 100.0%; Pred. No. 8e-42; Indels 0; Gaps 0;
	Matches 216; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
Qy	1 CCGCGCCGCCAGAGGGTGACTCAATCCAGGTGACAGCTCCAGCCATCTGGC 60
Db	2875 CCGCGCCGCCAGAGGGTGACTCAATCCAGGTGACAGCTCCAGCCATCTGGC 2934
Qy	61 CAGGCGTGAATGTCAGGAGCCAGCCATCAACGCTTACACTTGACAGGTG 120
Db	2935 CAGGCCTGACTGTCTGAGGCCAGCCATCAACGCTTACACTTGACAGGTG 2994
Qy	121 GGCGTGAAGCTACGCCCTCGTAAGCCGAGCTACCCCAACCATCTTGCTCC 180
Db	2995 GGCGTGAAGCTACGCCCTCGTAAGCCGAGCTACCCCAACCATCTTGCTCC 3054
Qy	181 CTTCACATCATGAGGCCAATGATGCGTGTACA 216
Db	3055 CTTCACATCATGAGGCCAATGATGCGTGTACA 3090
BASE COUNT	957 a 994 c 856 g 742 t 1 others
ORIGIN	
	Query Match 100.0%; Score 216; DB 6; Length 3550;
	Best Local Similarity 100.0%; Pred. No. 7.9e-42; Indels 0; Gaps 0;
	Matches 216; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
CDS	1. . 3093
	/note="unnamed protein product"
	/codon_start=1
	/protein_id="CAC09107.1"

QY 1 CCCCGCCGCCGCAAGGGGAGCTCATCCAGGTCACAGCTCCAGGATCTGC
Db 3532 CCGCGCCGCCCGCAGAGGGTGGACTCCATCCAGGTGACAGCTCCAGGATCTGC 3591
QY 61 CAGGCCGAGACTGCTCAGGCAGCCAGCCAGCTAACCGCTACACTCTGACAGGCG 120
Db 3592 CAGGCCGAGACTGCTCAGGCAGCCAGCTAACCGCTACACTCTGACAGGCG 3651
121 GGGCTGAACTGAGCCCTCGTAAGCGGAGTACCCCCAACCATTCCCTTGCTCCC 180
QY 3652 GGCTGAACTGAGCCCTCGTAAGCGGAGTACCCCCAACCATTCTTGCTCCC 3711
QY 181 CTTTCCACATCCATGAACGCCATGATCGTGACA 216
Db 3712 CTTTCCACATCCATGAACGCCATGATCGTGACA 3747

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Job time : 775.266 secs

Om nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:33:04 ; Search time 54.8323 Seconds
(without alignments)

Scoring table: IDENTITY_NUC GapOp 10.0 , Gapext 1.0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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21: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA2000.DAT:*

22: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA2001A.DAT:*

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searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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22: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA2001A.DAT:*

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24: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA2002.DAT:*

25: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/NA2003.DAT:*

RESULT 1 - AAD01234 standard; DNA: 216 BP.

XX AAD01234;

XX DT 04-OCT-2000 (first entry)

XX DE DNA encoding binding domain of human semaphorin 6A-1.

XX KW Human; semaphorin 6A-1; (HSA) SEM6A-1; neuronal development; apoptosis; neuronal regeneration; Ena/NASP protein family; immunomodulatory; gene therapy; diagnostic agent; therapeutic agent; differentiation; cytoskeletal stabilisation; plasticity; ds.

XX OS Homo sapiens.

XX FH Key CDS

FT FT Location/Qualifiers

FT FT 1..216

FT FT /*product= "Binding domain of semaphorin 6A-1"

FT FT /*tag= a

FT FT /*note= "The binding domain shows homology to zyxin protein and selectively binds to members of Ena/NASP protein family, especially Evi; the CDS does not include stop codon"

FT FT /*partial

XX PN WO20031252-A1.

XX PD 02-JUN-2000.

SUMMARIES

Result No. Score Match Length DB ID Description

1 216 100.0 216 21 AAD01234 DNA encoding bindi

2 216 100.0 1472 21 AAC98050 Human colon cancer

3 216 100.0 2123 22 AAK13995 Human full length

4 216 100.0 2227 22 AAK94365 Human cDNA for nov

5 216 100.0 2262 24 ABK34739 Human cDNA sequence

6 216 100.0 2293 22 AAK15834 Human cDNA sequence

7 216 100.0 2306 22 AAK17861 Human cDNA sequence

8 216 100.0 2592 23 AAS68253 DNA encoding novel

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

XX 26-NOV-1999; 99WO-EP09215.
 XX PR 26-NOV-1998; 98EP-0122441.
 XX PA (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.
 XX PI Behl C, Klostermann A;
 DR RPI; 2000-40005/34.
 XX PT P-PSDB; AAY71461.

XX PT Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent, therapeutic agent, for modulating immune system, in gene therapy or for effecting differentiation, cytoskeletal stabilization and/or plasticity
 PT -
 XX Claim 2; page 21; 53pp; English.

CC The present sequence is a DNA encoding binding domain of transmembraneous human semaphorin 6A-1 ((HSA)SEMA6-1) which is involved in neuronal development and regeneration mechanisms during apoptosis. The binding domain shows homology to Lyxin protein and selectively binds to members of Ena/VASP protein family, especially Evl. (HSA)SEMA6-1 is a member of protein family displaying secreted or transmembrane-based repulsive guidance cues critically involved in neuronal development.
 CC Expression of (HSA)SEMA6-1 is highest in embryonic brain and kidney and moderate in lung. The present sequence is useful as diagnostic and therapeutic agents, for modulating the immune system, in gene therapy, for effecting differentiation, cytoskeletal stabilisation and plasticity.
 XX Sequence 216 BP; 45 A; 85 C; 51 G; 35 T; 0 other;
 SQ Query Match 100.0%; score 216; DB 21; length 216;
 Best Local Similarity 100.0%; Pred. No. 2e-52; Matches 216; Conservative 0; Indels 0; Gaps 0;
 QY 1 CGCGCGGCCGCGCCGGAGAGGGTTGAGCTCCATCCAGGTGACAGCTCCAGGCATCTGGC 60
 Db 1 CGGCCGCGGCCGCCGGAGGGTGGACTCCATCCAGGTGACAGCTCCAGGCATCTGGC 60
 QY 61 CAGGCCGAGCTGTCGAGGGAGCCAGCCAGCTAACCTACACTGACTGACAAGGTGCG 120
 Db 61 CAGGCCGAGCTGTCGAGGGAGCCAGCCAGCTAACCTACACTGACTGACAAGGTGCG 120
 QY 121 GGCTGAGCTGAGCTGAGCTCTGAAACCGGAGTACCCCAAACATCCATTGCTGCC 180
 Db 121 GGCTGAGCTGAGCTGAGCTCTGAAACCGGAGTACCCCAAACATCCATTGCTGCC 180
 QY 181 CTTCCACATCCATGAGGCCCATGATGGCTGTACA 216
 Db 181 CTTCCACATCCATGAGGCCCATGATGGCTGTACA 216
 RESULT 2
 AAC98050
 ID AAC98050 standard; cDNA; 1472 BP.
 XX AAC98050;
 XX DT 09-MAR-2001 (first entry)
 DE Human colon cancer antigen nucleotide sequence SEQ ID NO:60.
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW identification; cytostatic; cardioactive; neuroprotective; vulnerability; immunomodulatory; muscular; gynecological; gastrointestinal; nephrotoxic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss.
 KW OS Homo sapiens.

XX WO2000055351-A1.
 XX PR 21-SEP-2000.
 XX PD 08-MAR-2000; 2000WO-US05883.
 XX PR 12-MAR-1999; 99US-0124270.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 DR WPI; 2000-587534/55.
 XX PR P-PSDB; AAB53293.
 XX Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
 XX PS Claim 1; page 510-511; 2104pp; English.
 XX AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB5234 to AAB54006. The human colon cancer antigens can have cyrotactic, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, pulmonary, nephrotropic, antifungal and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polypeptides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAC98773 represent sequences used in the exemplification of the present invention.
 XX Sequence 1472 BP; 437 A; 431 C; 299 G; 301 T; 4 other;
 SQ Query Match 100.0%; score 216; DB 21; length 1472;
 Best Local Similarity 100.0%; Pred. No. 3.2e-52; Matches 216; Conservative 0; Indels 0; Gaps 0;
 QY 1 CCCCGCGCGCCGCCGAGAGGGTTGACTCTCATCAGGGCAGCTCCAGGCCATCTGGC 60
 Db 372 CCCCGCGCGCCGCCGAGGGTTGACTCCATCAGGGCAGCTCCAGGCCATCTGGC 431
 QY 61 CAGCCGAGCTGAGCTGAGCTCTGAGGGAGCCAGCTAACCTACACTGACAAGGTGCG 120
 Db 432 CAGCCGAGCTGAGCTGAGCTCTGAGGGAGCCAGCTAACCTACACTGACAAGGTGCG 491
 QY 121 GGCTGAGCTGAGCTGAGCTCTGAAACCGGAGTACCCCAAACATCCATTGCTGCC 180
 Db 492 GGCTGAGCTGAGCTCTGAAACCGGAGTACCCCAAACATCCATTGCTGCC 551
 QY 181 CTTCCACATCCATGAGGCCCATGATGGCTGTACA 216
 Db 552 CTTCCACATCCATGAGGCCCATGATGGCTGTACA 587
 RESULT 3
 DE AAH13995
 ID AAH13995 standard; cDNA; 2123 BP.
 XX AC AAH13995;
 XX DT 26-JUN-2001 (first entry)
 XX DE Human cDNA sequence SEQ ID NO:11072.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX
OS HOMO sapiens.
XX EP1074617-A2.
PN XX
XX ID AAK94365 standard; cDNA; 2227 BP.
PD 07-FEB-2001.
XX PR 28-JUL-2000; 2000EP-0116126.
XX PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX PA (HELI-) HELIX RES INST.
XX PR Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.;
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T.;
XX DR WPI; 2001-318749/34.
XX PS Primer sets for synthesizing polynucleotides, particularly the 5602
full-length cDNAs defined in the specification, and for the detection
and/or diagnosis of the abnormality of the proteins encoded by the
full-length cDNAs -
XX Claim 8; SEQ ID 11072; 2537pp + CD ROM; English.
XX CC The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 3'-end sequence, where the
oligonucleotide comprises at least 15 nucleotides and the combination of
the 5'-end sequence is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
AAH1633 to AAH18742 represent human amino acid sequences; AAB92446 to
AAB9593 to AAB9593 represent human amino acid sequences; and AAH1362
represent oligonucleotides, all of which are used in the exemplification
of the present invention.
XX SQ Sequence 2123 BP; 550 A; 664 C; 528 G; 381 T; 0 other;
Query Match 100.0%; Score 216; DB 22; Length 2123;
Best Local Similarity 100.0%; Pred. No. 3.5e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC 1 CGCCCGCCGCCGCCGAGGGCTGGACATCCAGGTGACAGCUCCCAGCATCGGC 60
QY |||||||CGCGCGCCGCCGCCGAGGGCTGGACATCCAGGTGACAGCUCCCAGCATCGGC 1491
Db 1432 CGCCCGCCGCCGCCGAGGGCTGGACATCCAGGTGACAGCUCCCAGCATCGGC 1585
61 CAGGCCGTGACTGTCAGGAGGCCAGCCCTAACCTACACTGACAAGTCG 120
QY |||||||CGCGCGCCGCCGCCGAGGGCTGGACATCCAGGTGACAGCUCCCAGCATCGGC 1551
Db 1492 CGGCCGTGACTGTCAGGAGGCCAGCCCTAACCTACACTGACAAGTCG 1645
121 GGCTGAAGCTGACGCCCTGCGTAAGCGGAGGTACCCCCAACCATCCCTTGCC 180
QY |||||||GGCTGAAGCTGACGCCCTGCGTAAGCGGAGGTACCCCCAACCATCCCTTGCC 1552
Db 1646 GGCTGAAGCTGACGCCCTGCGTAAGCGGAGGTACCCCCAACCATCCCTTGCC 1705
181 CTTCACATCCATGAGGCCATGATGGCTACA 216
QY |||||||CTTCACATCCATGAGGCCATGATGGCTACA 1611
Db 1705 CTTCACATCCATGAGGCCATGATGGCTACA 1741

XX
OS HOMO sapiens.
XX EP1130094-A2.
PN XX PR 05-SEP-2001.
XX PR 07-JUL-2000; 2000EP-0114089.
XX PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-0118774.
PR 02-MAY-2000; 2000JP-0183765.
PA (HELI-) HELIX RES INST.
XX PI Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.;
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T., Koga, H.;
XX DR WPI; 2001-542425/58.
P-PSDB; AAM93444.
XX PT 830 Primers useful for synthesizing full length cDNA clones and their
use in genetic manipulation -
XX PS Claim 8; SEQ ID NO 3087; 1380pp + sequence listing; English.
CC The invention relates to primers for synthesising full length cDNA
clones. 830 cDNA molecules encoding a human protein have been
isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA
molecules have been determined. Primers for synthesising the full length
cDNA are useful for clarifying the function of the protein encoded by
the cDNA. The full length clones were obtained by construction of full
length enriched cDNA libraries that were synthesised by the oligo-capping
method. The primers enable the production of the full length cDNA easily
without any special methods. The present sequence is a full length
human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in CD-ROM format directly from EPO.
CC SQ Sequence 2227 BP; 567 A; 700 C; 560 G; 400 T; 0 other;
Query Match 100.0%; Score 216; DB 22; Length 2227;
Best Local Similarity 100.0%; Pred. No. 3.6e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC 1 CGCCCGCCGCCGCCGAGGGCTGGACATCCAGGTGACAGCUCCCAGCATCGGC 60
QY |||||||CGCGCGCCGCCGCCGAGGGCTGGACATCCAGGTGACAGCUCCCAGCATCGGC 1585
Db 1526 CGCCCGCCGCCGCCGAGGGCTGGACATCCAGGTGACAGCUCCCAGCATCGGC 1645
61 CAGGCCGTGACTGTCAGGAGGCCAGCCCTAACCTACACTGACAAGTCG 120
QY |||||||CGCGCGCCGCCGCCGAGGGCTGGACATCCAGGTGACAGCUCCCAGCATCGGC 1645
Db 1586 CGGCCGTGACTGTCAGGAGGCCAGCCCTAACCTACACTGACAAGTCG 1645
121 GGCTGAAGCTGACGCCCTGCGTAAGCGGAGGTACCCCCAACCATCCCTTGCC 180
QY |||||||GGCTGAAGCTGACGCCCTGCGTAAGCGGAGGTACCCCCAACCATCCCTTGCC 1705
Db 1646 GGCTGAAGCTGACGCCCTGCGTAAGCGGAGGTACCCCCAACCATCCCTTGCC 1705
181 CTTCACATCCATGAGGCCATGATGGCTACA 216
QY |||||||CTTCACATCCATGAGGCCATGATGGCTACA 1611
Db 1705 CTTCACATCCATGAGGCCATGATGGCTACA 1741

CC particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH01166 to AAH13628 and AAH1872 represent human cDNA sequences; AAH92445 to AAH13629 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX SQ sequence 2293 BP; 579 A; 713 C; 581 G; 420 T; 0 other;

Query Match 100 %; Score 216; DB 22; Length 2293;
Best Local Similarity 100 %; Pred. No. 3.6e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggcccccgcgcgcgaggggtggctccatcactcgatccgcattcgcc 60
Db 1608 cggcccccgcgcgcgaggggtggactccatcgatccgcacgtcc 1667

QY 61 CAGGGCGTGTGTCGAGGCGAGCCAGCCCTAACGCCTACACTGACAGGUG 120
Db 1668 CAGGGCGTGTGTCGAGGCGAGCCAGCCCTAACGCCTACACTGACAGGUG 1727

QY 121 GGCTGAAAGCGTACGCCATGAGCCATGATGCGCTACA 180
Db 1728 GGCTGAAAGCGTACGCCATGAGCCATGATGCGCTACA 216

QY 181 CTTCCACATCATGAAGCCAATGATGCGTGTACA 1823

RESULT 7

AAH17861 ID AAH17861 standard; cDNA; 2306 BP.
XX AAH17861;
AC XX DT 26-JUN-2001 (first entry)
XX DE Human cDNA sequence SEQ ID NO:17567.
XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX OS Homo sapiens.
XX PN EP1074617-A2.
XX PD 07-FEB-2001.
XX PF 28-JUL-2000; 2000EP-0116126.
XX PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118775.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J; Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX DR WPI; 2001-318749/34.

XX PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality or the proteins encoded by the full-length cDNAs -
XX PS Claim 8; SEQ ID 17567; 2537PP + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602

CC complements: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH01166 to AAH13628 and AAH13633 to AAH17861 represent human cDNA sequences; AAH92446 to AAH92445 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX SQ Sequence 2306 BP; 579 A; 739 C; 577 G; 411 T; 0 other;

Query Match 100 %; Score 216; DB 22; Length 2306;
Best Local Similarity 100 %; Pred. No. 3.6e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCCGCCGCCGCCGAGGGTGATCCATCGAGGTGACGCTCCAGGCCATCTGC 60
Db 1615 CGGCCGCCGCCGCCGCCGAGGGTGACTCCATCGAGGTGACGCTCCAGGCCATCTGC 1674

QY 61 CAGGGCGTGTGTCGAGGCGAGCCAGCCCTAACGCCTACACTGACAGGUG 120
Db 1675 CAGGGCGTGTGTCGAGGCGAGCCAGCCCTAACGCCTACACTGACAGGUG 1734

QY 121 GGCTGAAAGCGTACGCCATGAGCCATGATGCGCTACA 180
Db 1735 GGCTGAAAGCGTACGCCCTGCCTAACGCCGAGGTACCCCCAACACCATCTTGCTCC 1794

QY 181 CTTCCACATCATGAAGCCAATGATGCGTGTACA 216
Db 1795 CTTCCACATCATGAAGCCAATGATGCGTGTACA 1830

RESULT 8

AAS68253 ID AAS68253 standard; cDNA; 2592 BP.
XX AC AAS68253;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #4057.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PR 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0549167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;

DE DNA encoding novel human diagnostic protein #25525.

XX Human; chromosome mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX PR 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSEQ-) HYSEQ INC.

XX Dmancic RT; Liu C; Tang YI;

XX DR WPI; 2001-639362/73.

XX DR P-PSDB; ABB25534.

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

XX PS Claim 1; SEQ ID No 25525; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II), or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS4197-AAS94594 represent novel human diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 other;

SQ Query Match 100.0%; Score 216; DB 23; Length 3039; Best Local Similarity 100.0%; Pred. No. 3.8e-52; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CC CG CG CG CG CG CG AG AG GG GT GA CT CA TC AG CG CT CC AG CC AT C T G C 60

Db 2821 CC CG CG CG CG CG CG CA AG GG GT GA CT CA TC AG CG CT CC AG CC AT C T G C 2880

QY 61 CAG GCG GTG ACT GT GC TG AG GC AC CC AC CCT AC AG CT CA CT GA AG GRG 120

Db 2881 CAG GCG GTG ACT GT GC TG AG GC AC CC AC CCT AC AG CT CA CT GA AG GRG 2940

QY 121 GG CG TG AA CG GT AG CG CC CT CG TA AG CG CG AC CT TA CC CC CA AAC AC CA CT GT CG CC 180

Db 2941 GGG CT GA CG GT AG CG CC CT CG TA AG CG CG AC CT TA CC CC CA AAC AC CA CT GT CG CC 3000

QY 181 CTT T C C A C T C C A T G A G C C A A T G A T G C G T G C A 216

Db 3001 CTT T C C A C T C C A T G A G C C A A T G A T G C G T G C A 3036

XX RESULT 11

XX AAH17625

ID AAH17625 standard; cDNA; 3041 BP.

XX AC AAH17625;

XX DT 26-JUN-2001 (first entry)

XX DE Human cDNA sequence SEQ ID NO:17153.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.

XX PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.

XX PI Ota T; Isogai T; Nishikawa T; Bayashi K; Saito K; Yamamoto J;

PI Ishii S; Sugiyama T; Wakamatsu A; Nagai K; Otsuki T;

XX DR WPI; 2001-318749/34.

PT Primer sets for synthesizing Polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection of and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

XX PS Claim 8; SEQ ID 17153; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dR primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and the specific application. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH3628 and AAH13633 to AAH1842 represent human cDNA sequences; AAB9446 to AAS9583 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX SQ Sequence 3041 BP; 804 A; 886 C; 714 G; 637 T; 0 other;

Query Match 100.0%; Score 216; DB 22; Length 3041; Best Local Similarity 100.0%; Pred. No. 3.8e-52; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CG CG CG CG CG CG AG AG GG GT GA CT CA TC AG CG CT CC AG CC AT C T G C 60

Db 1966 CGGCCGCCCCGGCCGAGAGGGTGGACTCCATCCAGGTCAGACGCTCCAGCATCTGGC 2025
 QY 61 CAGGCCGTGACTGTCTCGAGSCAGGCCAGCCTCAAGCCCTACAATCTACAGCACAGGTC 120
 Db 2026 CAGGCCGTGACTGTCTCGAGGCCAGCCTCAAGCCCTACAATCTACAGCACAGGTC 2085
 QY 121 GGGCTGAAGCTTACCCCTGCTAAAGCCGACCTAACCATCTTGCTCC 180
 Db 2086 GGGCTGAAGCTTACCCCTGCTAAAGCCGACCTAACCATCTTGCTCC 2145
 QY 181 CTTTCACATCATGAGCCATAGCCAAACCATCTTGCTCC 216
 Db 2146 CTTTCACATCATGAGCCATAGCCAAACCATCTTGCTCC 2181

RESULT 12

AAA93618 AAA93618 standard; DNA; 3333 BP.

XX XX

AC AC

XX XX

DT DT

16-JAN-2001 (first entry)

DE DE

XX XX

Human semaphorin protein-like splice variant SECX 2864933-2 DNA.

KW KW

SECX protein; human; secreted; membrane-associated; cancer;

KW proliferation regulator; differentiation regulator; non-malignant tumour;

KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;

KW infection; inflammatory disorder; arthritis; haematopoietic disorder;

KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;

KW neurological disease; Alzheimer's disease; trauma; wounding;

KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;

KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;

KW neuroprotective; vulnerability; antiallergic; antimicrobial; cardiant;

KW dermatological; gene therapy; ds.

OS OS

Homo sapiens.

XX XX

PN PN

WO200053742-A2.

XX XX

PD PD

14-SEP-2000.

FF FF

09-MAR-2000; 2000WO-US06280.

XX XX

PR PR

09-MAR-1999; 990US-0123667.

XX XX

PA PA

(CURA-) CURAGEN CORP.

XX XX

PI PI

Shimkets RA;

XX XX

DR DR

WPI; 2000-594318/56.

P-PSDB; AAB23031.

XX XX

PT PT

Novel human membrane associated or secreted polypeptides and poly nucleotides useful for diagnosis, prevention and treatment of pathological states such as cancer, immune, cardiovascular and neurological disorders -

XX XX

PS PS

Claim 3; Fig 3; 15pp; English.

XX XX

CC CC

Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids which encode human SECX proteins (AAB3029-B23048). The SECX proteins

of the invention are either secreted or membrane-associated proteins and act as regulators of cellular proliferation and differentiation. SECX

proteins or nucleotides are useful for diagnosis the presence of, or predisposition to, a disease associated with altered levels of SECX

proteins and nucleotides. The SECX proteins are also useful to screen compounds that modulate SECX activity or expression. The interaction of a SECX protein with other cellular proteins may be useful to modulate the activity of a partner protein, cellular proliferation, cellular

differentiation and cell survival. SECX nucleotides are useful for the recombinant expression of SECX protein, and may be used detect SECX mRNA

CC CC

or genetic lesions in the SECX gene. They may also be used to modulate SECX expression (e.g., using antisense oligonucleotides). SECX nucleic acid sequences are also useful for identifying a cell or tissue type in a biological sample, and in forensic biology. SECX primers or probes are useful for detecting the presence of SECX nucleotides and for screening tissue cultures for contamination. Diseases that may be treated or prevented using SECX proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumours, immune disorders (including autoimmune diseases, transplant rejection, allergies, ATN), infections, inflammatory disorders, arthritis, haematoopoietic disorders, skin disorders, cardiovascular disorders, atherosclerosis, restenosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal disorders.

XX XX

SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 1 other;

Query Match Best Local Similarity 100.0%; Score 216; Length 3333; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2925 1 CCGCCGCCGCCGCCAGAGGGCTGACTCCATTAGGTGACAGCTCCAGCCTACAGCAGCAGCATCTGGC 2984

QY 61 CAGGCCGTGACTGTCTCGAGGCCAGCCAGCCTAACGCCCTACACTCACTGCAAGGTC 120

Db 2985 CAGGCCGTGACTGTCTCGAGGCCAGCCAGCCTAACGCCCTACACTGCAAGGTC 3044

QY 121 GGGCTGAAGCTTACGCCCTGCTAAAGCCGAGGTACCCCCAACCATCTTGCTCC 180

Db 3045 GGGCTGAAGCTTACGCCCTGCTAAAGCCGAGGTACCCCCAACCATCTTGCTCC 3104

QY 181 CTTTCACATCATGAGCCATAGATGCGTGTACA 216

Db 3105 CTTTCACATCATGAGCCATAGATGCGTGTACA 3140

RESULT 13

AAA93617 AAA93617

ID ID

AAA93617

XX XX

AC AC

XX XX

DT DT

16-JAN-2001 (first entry)

DE DE

Human semaphorin protein-like splice variant SECX 2864933-1 DNA.

XX XX

KW KW

SECX protein; human; secreted; membrane-associated; cancer;

KW proliferation regulator; differentiation regulator; non-malignant tumour;

KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;

KW infection; inflammatory disorder; arthritis; haematopoietic disorder;

KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;

KW neurological disease; Alzheimer's disease; trauma; wounding;

KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;

KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;

KW neuroprotective; vulnerability; antiallergic; antimicrobial; cardiant;

KW dermatological; gene therapy; ds.

OS OS

Homo sapiens.

XX XX

PN PN

WO200053742-A2.

XX XX

PD PD

14-SEP-2000.

FF FF

09-MAR-2000; 2000WO-US06280.

XX XX

PR PR

09-MAR-1999; 990US-0123667.

XX XX

PA PA

(CURA-) CURAGEN CORP.

XX XX

PI PI

Shimkets RA;

XX DR WPI; 2000-594318/56.
 XX DR P-PSDB; AAB23030.
 XX PT Novel human membrane associated or secreted polypeptides and poly nucleotides useful for diagnosis, prevention and treatment of pathological states such as cancer, immune, cardiovascular and neurological disorders -
 XX PS Claim 3; Fig 2; 15pp; English.
 XX CC Sequences AAA93616 A93631 and AAA93673-A93676 represent nucleic acids which encode human SECX proteins (AAB3029-B23008). The SECX proteins of the invention are either secreted or membrane-associated proteins and act as regulator of cellular proliferation and differentiation. SECX proteins or nucleotides are useful for diagnosing the presence of, or predisposition to, a disease associated with altered levels of SECX proteins and nucleotides. The SECX proteins are also useful to screen compounds that modulate SECX activity or expression. The interaction of a SECX protein with other cellular proteins may be useful to modulate the activity of a partner protein, cellular proliferation, cellular differentiation and cell survival. SECX nucleotides are useful for the recombinant expression of SECX protein, and may be used to detect SECX mRNA or genetic lesions in the SECX gene. They may also be used to modulate SECX expression (e.g., using antisense oligonucleotides). SECX nucleic acid sequences are also useful for identifying a cell or tissue type in a biological sample, and in forensic biology. SECX primers or probes are useful for detecting the presence of SECX nucleotides and for screening tissue cultures for contamination. Diseases that may be treated or prevented using SECX proteins or nucleotides include cancer (e.g., colorectal carcinoma, prostate cancer), benign tumours, immune disorders (including autoimmune diseases, transplant rejection, allergies, AIDS), infections, inflammatory disorders, arthritis, haematopoietic disorders, skin disorders, cardiovascular disorder, atherosclerosis, restenosis, neurological diseases (e.g., Alzheimer's disease), trauma (e.g., surgical or traumatic wounds, spinal cord injury), and skeletal disorders.
 XX SQ Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 1 other;
 Query Match 100.0%; Score 216; DB 21; Length 3498;
 Best Local Similarity 100.0%; Pred. No. 4e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 CCGCGCGCCGCCGCCAGAGGGTGCATCCAGTGACAGCTCCAGCCATCCTGGC 60
 Db 3090 CGCGCGCCGCCGCCAGAGGGTGCATCCAGTGACAGCTCCAGCCATCCTGGC 3149
 CC QY 61 CAGGGCGGTGACTGTCTGAGGGCACCCACCTGACGCTACACTCACTGAAAGGRC 120
 Db 3150 CAGGGCGGTGACTGTCTGAGGGCACCCACCTGACGCTACACTCACTGAAAGGRC 3209
 CC QY 121 GGGGTGAAGCTGAGCCATGCTAACGGGACTTACCCCAACCATCTTGTCCC 180
 Db 3210 GGCGCGAACGCTGAGCCCTGCTAACGGGACTTACCCCAACCATCTTGTCCC 3269
 CC QY 181 CTTCACATCCATGAGCCAACTGATGGGTGACA 216
 Db 3270 CTTCACATCCATGAGCCAACTGATGGGTGACA 3305
 XX RESULT 14
 AAV44295 ID AAV44295 standard; cDNA; 3550 BP.
 XX AC AAV44295;
 XX XX 06-OCT-1998 (first entry)
 DE Human secreted protein clone CJ145_1 cDNA.
 XX KW Secreted protein; human fetal brain; nutrition; cytokine; stimulant; cell proliferation; differentiation; immune system; suppressor; liaison;
 KW OS Homo sapiens.
 XX FT WO9227205-A2.
 PN XX
 FT XX
 PD 25-JUN-1998.
 XX PR 17-DEC-1997; 97WO-US23330.
 PF XX
 PR 16-DEC-1997; 97US-0991872.
 PR 18-DEC-1996; 96US-079192.
 PR 13-JAN-1997; 97US-0783401.
 PA XX
 PA (GEMY) GENETICS INST INC.
 XX PI Agostino MJ, Jacobs K, Larallie ER, McCoy JM, Merberg D;
 PT Racie LA, Spaulding V, Treacy M;
 PT XX
 DR WPI; 1998-362774/31.
 DR P-PSDB; AAW64221.
 PS XX
 PT New polynucleotides and secreted proteins - obtained from human foetal brain, human adult testes, human adult brain and human adult salivary gland cDNA libraries
 PT XX
 DR WPI; 1998-362774/31.
 DR P-PSDB; AAW64221.
 PS XX
 CC SQ Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other;
 CC CC This sequence encodes a novel secreted protein from clone CJ145_1 isolated from a human fetal brain cDNA library. This protein has applications for nutritional use, cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, hematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombotic activity, receptor/ligand activity, anti-inflammatory activity, catheelin/tumour invasion suppressor activity, tumour inhibition activity and other activities.
 CC XX SQ Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other;
 CC CC Query Match 100.0%; Score 216; DB 19; Length 3550;
 Best Local Similarity 100.0%; Pred. No. 4e-52;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 CCGCGCCGCCGCCAGAGGGTGCATCCAGTGACAGCTCCAGCCATCTGGC 60
 Db 2835 CGCGCGCCGCCGCCAGAGGGTGCATCCAGTGACAGCTCCAGCCATCTGGC 2894
 CC QY 61 CAGGGCGGTGACTGTCTGAGGGCACCCACCTGACGCTACACTCACTGAAAGGRC 120
 Db 2895 CAGGGCGGTGACTGTCTGAGGGCACCCACCTGACGCTACACTCACTGAAAGGRC 2954
 CC QY 121 GGCGCGAACGCTGAGCCCTGCTAACGGGACTTACCCCAACCATCTTGTCCC 180
 Db 2955 GGCGCGAACGCTGAGCCCTGCTAACGGGACTTACCCCAACCATCTTGTCCC 3014
 CC QY 181 CTTCACATCCATGAGCCAACTGATGGGTGACA 216
 Db 3015 CTTCACATCCATGAGCCAACTGATGGGTGACA 3050
 XX RESULT 15
 AAF98469 ID AAF98469 standard; cDNA; 3550 BP.
 XX XX

Search completed: September 30, 2003. 16:58:39
 Job time : 59.8323 secs

AC AAF98469;
 XX
 XX DT 07-JUN-2001 (first entry)
 XX DE Human cDNA clone CJ145_1 sequence SEQ ID 160.
 XX KW Human; secreted protein; nutrient; cytokine modulator; proliferation; differentiation; immune system modulator; tissue growth; chemotactic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 KW XX haemopoiesis.
 OS Homo sapiens.
 XX PN WO200119988-A1.
 XX PD 22-MAR-2001.
 XX PR 14-SEP-2000; 2000WO-US25135.
 XX 17-SEP-1999; 99US-0398829.
 PA (GEMY) GENETICS INST INC.
 XX PT Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Tracy M, Bowman MR, Spaulding W, Agostino MJ;
 XX DR WPI; 2001-244801/25.
 DR P-PSDB; AAB0731.
 XX PT Isolated nucleic acids encoding polypeptides, useful for modulating immune system and hematopoiesis regulating activity -
 PT Disclosure; Page 486-487; 557pp; English.
 XX CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted proteins AAF9057 - AAF90750. The cDNA clones are isolated from various tissue types, and may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate protein expression. The polypeptides and nucleic acids may be used as nutrients or to modulate cytokine and cell proliferation/differentiation activity and may also be involved in modulation of the immune system. The cDNA sequences, proteins, their agonists and/or antagonists exhibit haemopoiesis, regulating activity; tissue growth activity; activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic activity; receptor/ligand activity; anti-inflammatory activity; haemopoiesis activity; cadherin/tumour suppressor activity; and/or tumour inhibition activity. Included in the invention are probes represented in AAF98490 - AAF98572 which are specific for the cDNA clones encoding the secreted proteins.
 CC XX Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other;
 SQ Query Match 100.0%; Score 216; DB 22; Length 3550;
 Best Local Similarity 100.0%; Pred. No. 4e-52; Mismatches 0; Indels 0; Gaps 0;
 Matches 216; Conservative 0;
 QY 1 CCGCCGCCGCCGCCAGGGGGCATCCATCCAGGTGACAGCTCCAGGCATC 60
 Db 2835 CCGCCGCCGCCGCCAGGGGGCATCCATCCAGGTGACAGCTCCAGGCATC 2894
 QY 61 CAGGCCGAGCTGCTGAGGCCAGCCAGCTAACGCTAACACTGACAGTCG 120
 Db 2895 CAGGCCGAGCTGCTGAGGCCAGCCAGCTAACGCTAACACTGACAGTCG 2954
 QY 121 GGCTGAGGTAGCCCTGCCTAAAGCGGAGTAACCCCAACCATCCTTGCCC 180
 Db 2955 GGCTGAGGTAGCCCTGCCTAAAGCGGAGTAACCCCAACCATCCTTGCCC 3014
 QY 181 CTTCCTCACATCCATGAAGCCAAATGATGCGTGTACA 216
 Db 3015 CTTCCTCACATCCATGAAGCCAAATGATGCGTGTACA 3050

OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:36:23 ; Search time 14,4914 Seconds

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GenCore version 5.1.6

Title: US-09-856-681-3

Perfect score: 216

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/podata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	35.4	16.4	1971	US-08-818-253-7
C 2	35.4	16.4	1971	US-08-818-253-7
C 3	35.2	16.3	13987	US-08-804-227C-13
C 4	35.2	16.3	43280	US-08-804-227C-1
C 5	34.4	15.9	4403765	US-09-103-940A-2
C 6	34.4	15.9	4411529	US-09-103-940A-2
C 7	33.8	15.6	846	US-09-252-991A-1737
C 8	33.8	15.6	1026	US-09-252-991A-1737
C 9	33.8	15.6	2667	US-09-252-991A-1954
C 10	33.8	15.6	3228	US-09-252-991A-1816
C 11	33.8	15.6	3228	US-09-252-991A-2143
C 12	33.2	15.4	630	US-09-252-991A-7012
C 13	33.2	15.4	1581	US-09-252-991A-7061
C 14	33.2	15.4	1581	US-09-252-991A-7117
C 15	33	15.3	1536	US-08-993-359-29
C 16	33	15.3	1536	US-09-482-559A-29
C 17	32	1153	2	US-08-889-793-5
C 18	32	14.8	1162	US-09-620-312D-982
C 19	31.8	14.7	1119	US-09-170-496D-65
C 20	31.8	14.7	1119	US-09-170-496D-199
C 21	31.8	14.7	1679	US-08-202-056-6
C 22	31.8	14.7	1679	US-08-076-093A-5
C 23	31.8	14.7	1679	US-08-071-263-5
C 24	31.8	14.7	1679	US-08-284-589-5
C 25	31.8	14.7	1679	US-08-805-478-5
C 26	31.8	14.7	1679	US-08-801-238-5
C 27	14.7	1679	2	US-08-801-238-5

RESULT 1
US-08-818-253-7/c
; Sequence 7, Application US/08818253
; Patent No. 5938204
; Sequence 7, Application US/08818253
GENERAL INFORMATION:
APPLICANT: Mizwaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,253
FILING DATE: 14-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-0999
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1971 base Pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1968
,
/US-08-818-253-7

Query Match Score 16.4%; DB Best Local Similarity 61.3%; Pred. No. 0.31; Matches 57; Conservati 0; Mismatches 0;

Sequence 3', Appli
Sequence 5', Appli
Sequence 3', Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 751, Ap
Sequence 976, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 3, Appli
Sequence 21, Appli
Sequence 1, Appli
Sequence 786, Ap
Sequence 10, Appli
Sequence 10864, A
Sequence 10820, A

QY 2 CGCCGCCGCCGCCAGGGGGGATCAGTCAGCTGCAGCCATCTGGCC 61
 NAME: Plant, Thomas, G.
 Db 112 CGCCGCCAGGTGACGGTGCACGGTGCACGCCCTCGCCCTGCTCA 53
 REGISTRATION NUMBER: 35,784
 REFERENCE/DOCKET NUMBER: X-8231
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 317-276-2459

RESULT 2
 US-08-818-252-7/c
 ; Sequence 7, Application US/08818252B
 ; Patent No. 6197928
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsien, Roger Y.
 ; APPLICANT: Miyawaki, Atsushi
 ; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
 ; DETECTION OF ANALYTES
 ; FILE REFERENCE: 07257/042001
 ; CURRENT APPLICATION NUMBER: US/08/818, 252B
 ; CURRENT FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 7
 ; LENGTH: 1971
 ; TYPE: DNA
 ; ORGANISM: Aequorea victoria
 ; FEATURE:
 ; LOCATION: CDS
 ; NAME/KEY: CDS
 ; LOCATION: (0) .. (1968)
 ; US-08-818-252-7

Query Match 16.4%; Score 35.4; DB 3; Length 1971;
 Best Local Similarity 61.3%; Pred. No. 0.31; Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Length: 1971

QY 2 CGCCGCCGCCGCCAGGGGGACTCCATCCAGGTGCACAGCTCCAGCATCTGGCC 61
 Db 1346 CGCCGAGGGGTGTCGGCGCGTGTCCCCCGCCAGGAGGGCCAGTGCC 1287
 QY 62 AGCCGCGTGAATGTTGAGGAGCCAGCTAACGCTTCAAGCTCCAGCATCTGGCC 61
 Db 1286 CGCCCTCGAGGGGTGCGGGCGGGGTTGGGTCCTGAGCTGACGTAGCGGACGG 1227
 QY 122 GCUTGAAGGTACGCCCTGCTAAAGCCGACCAACCCCCAACATCTTGTCCC 181
 Db 1226 CGCCGGTGTGACGCCGCCGGTAGGCCTGGCAGAGCTTCTGGCTCC 1167
 QY 182 TTTCACATCCATGAGGCC 201
 Db 1166 GTCGGGAGTGTGAGGCC 1147

RESULT 3
 US-08-804-227C-13/c
 ; Sequence 13, Application US/08804227C
 ; Patent No. 5876991
 ; GENERAL INFORMATION:
 ; APPLICANT: DeHoff, Bradley S.
 ; APPLICANT: Kuhstoss, Stuart A.
 ; APPLICANT: Rostek, Paul R., Jr.
 ; APPLICANT: Sutton, Kimberly L.
 ; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Thomas G. Plant 1501
 ; STREET: LILLY CORPORATE CENTER
 ; CITY: INDIANAPOLIS
 ; STATE: IN
 ; COUNTRY: USA
 ; ZIP: 46285
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: ASCII(DOS) Text only
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/804 227C
 ; FILING DATE: February 21, 1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plant, Thomas, G.
 ; REGISTRATION NUMBER: 35,784
 ; REFERENCE/DOCKET NUMBER: X-8231
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 317-276-2459
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13987 base Pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 350..13987
 ; US-08-804-227C-13

Query Match 16.3%; Score 35.2; DB 2; Length 13987;
 Best Local Similarity 48.5%; Pred. No. 0.58; Matches 97; Conservative 0; Mismatches 103; Indels 0; Gaps 0; Length: 13987

QY 2 CGCCGCCGCCGCCAGGGGGACTCCATCCAGGTGCACAGCTCCAGCATCTGGCC 61
 Db 1346 CGCCGAGGGGTGTCGGCGCGTGTCCCCCGCCAGGAGGGCCAGTGCC 1287
 QY 62 AGCCGCGTGAATGTTGAGGAGCCAGCTAACGCTTCAAGCTCCAGCATCTGGCC 61
 Db 1286 CGCCCTCGAGGGGTGCGGGCGGGGTTGGGTCCTGAGCTGACGTAGCGGACGG 1227
 QY 122 GCUTGAAGGTACGCCCTGCTAAAGCCGACCAACCCCCAACATCTTGTCCC 181
 Db 1226 CGCCGGTGTGACGCCGCCGGTAGGCCTGGCAGAGCTTCTGGCTCC 1167
 QY 182 TTTCACATCCATGAGGCC 201
 Db 1166 GTCGGGAGTGTGAGGCC 1147

RESULT 4
 US-08-804-227C-1/c
 ; Sequence 1, Application US/08804227C
 ; Patent No. 5876991
 ; GENERAL INFORMATION:
 ; APPLICANT: DeHoff, Bradley S.
 ; APPLICANT: Kuhstoss, Stuart A.
 ; APPLICANT: Rostek, Paul R., Jr.
 ; APPLICANT: Sutton, Kimberly L.
 ; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Thomas G. Plant 1501
 ; STREET: LILLY CORPORATE CENTER
 ; CITY: INDIANAPOLIS
 ; STATE: IN
 ; COUNTRY: USA
 ; ZIP: 46285
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: ASCII(DOS) Text only
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/804 227C
 ; FILING DATE: February 21, 1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plant, Thomas, G.
 ; REGISTRATION NUMBER: 35,784
 ; REFERENCE/DOCKET NUMBER: X-8231
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 317-276-2459
 ; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 43280 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 816..14234
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 14351..19945
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 20101..31199
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 31232..36067
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 36249..41774
 US-08-804-227C-1

RESULT 6
 Query Match 16.3%; Score 35.2; DB 2; Length 43280;
 Best Local Similarity 48.5%; Pred. No. 0; 78; Mismatches 103; Indels 0; Gaps 0;
 Matches 97; Conservative

QY 2 CGCGCGCGCCCGCAGAGGGTGACTCATCAGTGACAGCTCCAGCATCTGCC 61
 Db 1896 CGCGGAGCGCGCGCTCGGCCCGCTGTGCGGCCCGGCCGAGCAGCGCCAGTGG 1837

QY 62 AGGCCGACTGCTCCAGGCCAGCTCACGCTACACTCACTGACAGGTGG 121
 Db 1836 CGCGCTCAGCGGGTCAGCGGGCGCGGGGAGCTCGTGACTCCAGTGGAAGG 1777

QY 122 GGCTGAAGCTGACGCCCTCGCTAAAGCGGACCTACGCCAACCAACCATATGCTCCC 181
 Db 1776 CGCGGGCTGACGCCCTCGCTAAAGCGGACCTACGCCAACCAACCATATGCTCCC 1717

QY 182 TTRCCACATCCATGAAACC 201
 Db 1716 GGCAGGGAGTGGTGGAGCGC 1697

RESULT 5
 US-09-103-840A-2/c
 Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103, 840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
 LENGTH: 4411529
 TYPE: DNA
 ORGANISM: Mycobacterium tuberculosis
 OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match 15.9%; Score 34.4; DB 3; Length 4411529;
 Best Local Similarity 49.2%; Pred. No. 0.72; Mismatches 92; Indels 0; Gaps 0;
 Matches 89; Conservative

QY 22 GTGGACTCATCCAGGTGACAGCTCCAGCCATCTGGCAGGCCGTACTGCTCGAGG 81
 Db 744035 GGTTATTCTCGTAGAGGCCACACTCGTGGCTACCCGGCGCGGCACTGGCG 7433976

QY 82 CAGCCAGCTCAAGCCCTACAATCACTGACAGTGGGGTGAAG 129
 Db 743975 CGGTCCTGCACCAAGCGACGACAAAGCCCCCACGCTGGGGTGAAG 743928

RESULT 7
 US-09-252-991A-8905/c
 Sequence 8905, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074, 788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094, 190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 8905
 ; LENGTH: 846
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-8905

Query Match 15.6%; Score 33.8; DB 4; Length 846;
 Best Local Similarity 49.2%; Pred. No. 0.72; Mismatches 92; Indels 0; Gaps 0;
 Matches 89; Conservative

QY 2 CGGGCCGCCCGCAGAGGGTGGACTCATCCAGGTGACAGCTCCAGCCATCTGCC 61

RESULT 8
US-01-252-991A-1737
; Sequence 1737, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: MARC J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196-136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIORITY NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 1737

; LENGTH: 1026

; TYPE: DNA

; ORGANISM: *Pseudomonas aeruginosa*

US-03-252-991A-1737

Query Match 15 6%; Score 33 8; DB 4; Length 1026;
Best Local Similarity 54 4%; Fred. No. 0.76; Mismatches 0; Indels 0; Gaps 0;

Matches 68; Conservative 0; MisMatches 0; Del 0; Insert 0;

QY 62 AGGCCGTGACTGTCTGGAGCCAGCCAGCTAACACTCACTGACAAAGGTGG 121
Db 271 AGCCGGATCACACCAAGGAAGTCTGAGCGAAGGCAAGGA 330

QY 122 GGCTGAAGCTACGCCCTGCTTAAGCCGACGTACCCCAAACCATCTTGTCTCCC 181
Db 331 GAAGGAAGAGGCCAACRAGGGGCCGCCTGACACTTATCAGCTGGCGGCG 390

QY 182 TTTC 186
Db 391 TTAC 395

RESULT 9
US-09-252-991A-9254
; Sequence 9254, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196-136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIORITY NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 9254

; LENGTH: 2667

RESULT 10
US-09-252-991A-1816
; Sequence 1816, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: MARC J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196-136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIORITY NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 1816

; LENGTH: 3228

; TYPE: DNA

; ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-1816

Query Match 15 6%; Score 33 8; DB 4; Length 3228;
Best Local Similarity 54 4%; Fred. No. 1; Mismatches 0; Indels 0; Gaps 0;

Matches 68; Conservative 0; MisMatches 0; Del 0; Insert 0;

QY 62 AGCCGTGACTGTCTGGAGCCAGCCAGCTAACACTCACTGACAAAGGTGG 121
Db 303 AGCCGGATCACACCAAGGAAGTCTGAGCGAAGGCCAGGA 362

QY 122 GGCTGAAGCTACGCCCTGCTTAAGCCGACGTACCCCAAACCATCTTGTCTCCC 181
Db 363 GAAGGAAGAGGCCAACRAGGGGCCGCCTGACACTTATCAGCTGGCGGCG 422

QY 182 TTTC 186
Db 423 TTAC 427

RESULT 11
US-09-252-991A-2143/c
; Sequence 2143, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196-136

RESULT 15
 US-08-993-359-29
 ; Sequence 29, Application US/08993359A
 ; Patent No. 6039942
 ; GENERAL INFORMATION:
 ; APPLICANT: Lassen, Soren F.
 ; APPLICANT: Bech, Lisbeth
 ; APPLICANT: Ohmann, Anders
 ; APPLICANT: Breinholt, Jens
 ; APPLICANT: Fuglsang, Claus C.
 ; APPLICANT: Ostergaard, Peter R.
 TITLE OF INVENTION: Phytase Polypeptides
 FILE REFERENCE: 5383_500-US
 CURRENT APPLICATION NUMBER: US/08/993_359A
 CURRENT FILING DATE: 1997-12-18
 EARLIER APPLICATION NUMBER: 1480/96
 EARLIER FILING DATE: 1996-12-20
 EARLIER APPLICATION NUMBER: 1481/96
 EARLIER FILING DATE: 1996-12-20
 EARLIER APPLICATION NUMBER: 0301/97
 EARLIER FILING DATE: 1997-03-18
 EARLIER APPLICATION NUMBER: 0529/97
 EARLIER FILING DATE: 1997-05-07
 EARLIER APPLICATION NUMBER: 1388/97
 EARLIER FILING DATE: 1997-11-01
 EARLIER APPLICATION NUMBER: 60/046,082
 EARLIER FILING DATE: 1997-05-09
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 29
 LENGTH: 1536
 TYPE: DNA
 ORGANISM: Trametes pubescens
 FEATURE:
 NAME/KEY: CDS
 NAME/KEY: mat_peptide
 LOCATION: (79)..(1407)
 LOCATION: (130)..(1407)
 NAME/KEY: sig_peptide
 LOCATION: (79)..(129)
 US-08-993-359-29

Query Match 15.3%; Score 33; DB 3; Length 1536;
 Best Local Similarity 53.5%; Pred. No. 1,4; Mismatches 0; Indels 0; Gaps 0;
 Matches 69; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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QY          11 CCCCGCAGGGGAGCTCCATCCAGGAGCTACGCTCCAGCATCTGGCCAGGCCCTGA 70
Db          950 CCGTGCAGGCCTGGTACATCACCGAGCTCATGGCCGCCCTACCGCCGAGACGTGT 1009
QY          71 CGCTCTCAGGGAGCCAGCTCAACCTAACCTACTGACAAGTCGGGCTGAGC 130
Db          1010 CCGACACACGAGACAGCACACTGACTCTGCCCCAGACGCTCCGCTCAACC 1069
QY          131 GTAGCCCT 139
Db          1070 GCACGCTT 1078

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Search completed: September 30, 2003, 22:06:17
 Job time : 27.4914 secs

Gencore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:

September 30, 2003, 16:44:06 ; Search time 53.2004 Seconds

{without alignments} 10107.639 Million cell updates/sec

Title: us-09-856-681-3

Perfect score:

216

Sequence: 1 cgcgcggccqcccqagag.....agccaatgtatgttgtaca 216

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

Post-processing: Minimum Match 0%

Maximum DB seq length: 200000000

Post-processing: Maximum Match 100%

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Database : Published Applications N/A:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	216	100.0	3333	11 US-09-937-187-5
5	216	100.0	3498	11 US-09-991-053-3
6	216	100.0	3498	11 US-09-957-187-3
7	216	100.0	4250	11 US-09-957-187-4
8	168	77.8	460	11 US-09-918-995-3799
9	55	25.5	6767	11 US-09-774-891-6944
10	55	25.5	6773	11 US-09-764-891-6943
11	53.4	24.7	662	11 US-09-64-891-810
12	37.4	17.3	765	13 US-10-027-632-16626
13	35.4	16.4	1971	10 US-09-554-000-7
14	35.2	16.3	936	14 US-10-128-714-2578
15	35.2	16.3	936	14 US-10-128-714-2578
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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database : Published Applications N/A:*

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RESULT 1

Sequence 60, Application US/09925299

Patent No. US20020055627A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09925-299

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124, 270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1156

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 60

LENGTH: 1472

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: misc_feature

NAME/KEY: misc_feature

LOCATION: (1129)

OTHER INFORMATION: n equals a,t,g, or c

NAME/KEY: misc_feature

LOCATION: (1130)

OTHER INFORMATION: n equals a,t,g, or c

US-09-925-299-60

Query Match

Best Local Similarity

Matches 216, Conservative

Score 100.0%, Prcd. No. 5.1e-58;

Mismatches 0; Indels 0; Gaps 0;

Sequence 310, App

Sequence 166826, App

Sequence 7, App

Sequence 2578, App

Sequence 7578, App

Sequence 1578, App

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Qy 1 CGCCGCGCCGCCGCCAGGGGGGACTCATCCAGGGCACACTCCAGCAGCTGGC 60
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Db 372 CGCGCCGCCGCCAGGGGTGACTCCATCAGGTGACAGCTCCAGCCATCTGGC 431

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; RESULT 2
; US-09-925-299-60
; Sequence 60, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925, 299
; CURRENT FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: PCT/US00/05883
; PRIORITY FILING DATE: 2000-03-08
; PRIORITY APPLICATION NUMBER: 60/124, 270
; PRIORITY FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-299-60

Query Match          100.0%; Score 216; DB 11; Length 1472;
Best Local Similarity 100.0%; Pred. No. 5.1e-58; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; RESULT 3
; US-09-991-053-5
; Sequence 5, Application US/0991053
; Publication No. US2003003532A1
; GENERAL INFORMATION:
; APPLICANT: Shmikets, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-1, -2, AND ROUNDABOUT-LIKE POLYPEPTIDES
; FILE REFERENCE: 1556-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991, 053
; CURRENT FILING DATE: 2002-05-23
; PRIORITY APPLICATION NUMBER: USN 60/123, 667

; RESULT 3
; US-09-991-053-5
; Sequence 5, Application US/0991053
; Publication No. US2003003532A1
; GENERAL INFORMATION:
; APPLICANT: Shmikets, Richard A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-1, -2, AND ROUNDABOUT-LIKE POLYPEPTIDES
; FILE REFERENCE: 1556-540 CON S-10
; CURRENT APPLICATION NUMBER: US/09/991, 053
; CURRENT FILING DATE: 2002-05-23
; PRIORITY APPLICATION NUMBER: USN 60/123, 667

; RESULT 4
; US-09-957-187-5
; Sequence 5, Application US/09957187
; Publication No. US2003005454A1
; GENERAL INFORMATION:
; APPLICANT: Shmikets, Richard A.
; APPLICANT: LaRochelle, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 1556-540 CIP
; CURRENT APPLICATION NUMBER: US/09/957, 187
; CURRENT FILING DATE: 2000-09-19
; PRIORITY APPLICATION NUMBER: 60/123, 667
; PRIORITY FILING DATE: 1999-03-09
; PRIORITY APPLICATION NUMBER: 09/520, 781
; PRIORITY FILING DATE: 2000-03-03
; PRIORITY APPLICATION NUMBER: 60/234, 082
; PRIORITY FILING DATE: 2000-09-20
; PRIORITY APPLICATION NUMBER: 60/233, 798
; PRIORITY FILING DATE: 2000-09-19
; PRIORITY APPLICATION NUMBER: 60/174, 485
; PRIORITY FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: cds
; NAME/KEY: (214)..(2865)
; LOCATION: (2882)
; OTHER INFORMATION: an n may be any one of a or t or g or c
; US-09-957-187-5

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Query Match 100.0%; Score 216; DB 11; Length 3333; US-09-957-187-3
 Best Local Similarity 100.0%; Pred. No. 5.5e-58; Sequence 3, Application US/09957187
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Publication No. US20030054514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shinkets, Richard A.
 ; ATTORNEY: LaRochelle, William
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
 ; FILE REFERENCE: 15966-540 CIP
 ; CURRENT APPLICATION NUMBER: US/09/957,187
 ; CURRENT FILING DATE: 2000-09-19
 ; PRIORITY APPLICATION NUMBER: 60/123,667
 ; PRIORITY FILING DATE: 1999-03-09
 ; PRIORITY APPLICATION NUMBER: 09/520,781
 ; PRIORITY FILING DATE: 2000-03-03
 ; PRIORITY APPLICATION NUMBER: 60/234,082
 ; PRIORITY FILING DATE: 2000-09-20
 ; PRIORITY APPLICATION NUMBER: 60/233,798
 ; PRIORITY FILING DATE: 2000-09-19
 ; PRIORITY APPLICATION NUMBER: 60/174,485
 ; PRIORITY FILING DATE: 2000-01-04
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 LENGTH: 3498
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (214)..(3030)
 NAME/KEY: misc_feature
 LOCATION: (3047)
 OTHER INFORMATION: an n may be any one of a or t or g or c
 ; US-09-957-187-3
 Query Match 100.0%; Score 216; DB 11; Length 3498;
 Best Local Similarity 100.0%; Pred. No. 5.5e-58; Sequence 3, Application US/09957187
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Publication No. US20030054514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shinkets, Richard A.
 ; ATTORNEY: LaRochelle, William
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
 ; FILE REFERENCE: 15966-540 CIP
 ; CURRENT APPLICATION NUMBER: US/09/957,187
 ; CURRENT FILING DATE: 2000-09-19
 ; PRIORITY APPLICATION NUMBER: 60/123,667
 ; PRIORITY FILING DATE: 1999-03-09
 ; PRIORITY APPLICATION NUMBER: 09/520,781
 ; PRIORITY FILING DATE: 2000-03-03
 ; PRIORITY APPLICATION NUMBER: 60/234,082
 ; PRIORITY FILING DATE: 2000-09-20
 ; PRIORITY APPLICATION NUMBER: 60/233,798
 ; PRIORITY FILING DATE: 2000-09-19
 ; PRIORITY APPLICATION NUMBER: 60/174,485
 ; PRIORITY FILING DATE: 2000-01-04
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 3
 LENGTH: 3498
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (214)..(3030)
 NAME/KEY: misc_feature
 LOCATION: (3047)
 OTHER INFORMATION: an n may be any one of a or t or g or c
 ; US-09-957-187-3
 Query Match 100.0%; Score 216; DB 11; Length 3498;
 Best Local Similarity 100.0%; Pred. No. 5.5e-58; Sequence 3, Application US/09957187
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Publication No. US20030054514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shinkets, Richard A.
 ; ATTORNEY: LaRochelle, William
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
 ; FILE REFERENCE: 15966-540 CIP
 ; CURRENT APPLICATION NUMBER: US/09/957,187
 ; CURRENT FILING DATE: 2000-09-19
 ; PRIORITY APPLICATION NUMBER: 60/123,667
 ; PRIORITY FILING DATE: 1999-03-09
 ; PRIORITY APPLICATION NUMBER: 09/520,781
 ; PRIORITY FILING DATE: 2000-03-03
 ; PRIORITY APPLICATION NUMBER: 60/234,082

PRIOR APPLICATION NUMBER: 60/233,798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174,485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 84
LENGTH: 4250
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (250)..(3390)
; US-09-957-187-84

RESULT 8
US-09-918-995-3799/C
; Sequence 3799, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED FROM VARIOUS DNA LIBRARIES
; FILE REFERENCE: 20411-56
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 3799
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(460)
; OTHER INFORMATION: n = A,T,C or G
; US-09-918-995-3799

Query Match 100 %; Score 216; DB 11; Length 4250;
Best Local Similarity 100 %; Pred. No. 5; 7e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; US-09-957-187-84

QY 1 CGGCCGCGCCGGAGGGTGGACTCCATCCAGGTGACAGCTCCAGCCATCTGGC 60
Db 3175 CGGCCGCGCCGGAGGGTGGACTCCATCCAGGTGACAGCTCCAGCCATCTGGC 3234

QY 61 CAGGCCGAGCTGCTGAGGCTGCTAAGCCGAGTCAGCCCCAACATCACCTTGCTCC 120
Db 3235 CAGGCCGAGCTGCTGAGGCTGCTAAGCCGAGTCAGCCCCAACATCACCTTGCTCC 3294

QY 121 GGCTGAGCTGCTGAGGCTGCTAAGCCGAGTCAGCCCCAACATCACCTTGCTCC 180
Db 3295 GGCTGAGCTGCTGAGGCTGCTAAGCCGAGTCAGCCCCAACATCACCTTGCTCC 3354

QY 181 CTTCCACATCCATGAAGCCCATTGATGCCGTACCA 216
Db 3355 CTTCACACATCCATGAAGCCCATTGATGCCGTACCA 3390

RESULT 9
US-09-764-891-6944
; Sequence 6944, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6943
; LENGTH: 6767
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-891-6944

Query Match 25.5%; Score 55; DB 11; Length 6767;
Best Local Similarity 64.6%; Pred. No. 1; 4e-07;
Matches 82; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
; US-09-764-891-6944

QY 74 TCTCGAGGCCAGCTCAAGCTTACAACCTACTGACAGCTGCGGGCTGAAAGTA 133
Db 5521 TCTCGAGGCCAGCTCAAGCTTACAACCTACTGACAGCTGCGGGCTGAAAGTA 5580

QY 134 CGCCCTCTGCTAAAGCCGAGGACCCCCAACATCCTTGCCTCCCTTACATCCA 193
Db 5581 CGCCCTCTGCTAAAGCCGAGGACCCCCAACATCCTTGCCTCCCTTACATCCA 5640

QY 194 TGAGGCC 200
Db 5641 TAGACC 5647

RESULT 10
US-09-764-891-6943
; Sequence 6943, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 6943
; LENGTH: 6773
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-764-891-6943

Query Match 25.5%; Score 55; DB 11; Length 6773;
Best Local Similarity 64.6%; Pred. No. 1; 4e-07;
Matches 82; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
; US-09-764-891-6943

QY 74 TCTCGAGGCCAGCTCAAGCTTACAACCTACTGACAGCTGCGGGCTGAAAGTA 133
Db 5527 TCTCGAGGCCAGCTCAAGCTTACAACCTACTGACAGCTGCGGGCTGAAAGTA 5586

QY 134 CGCCCTCTGCTAAAGCCGAGGACCCCCAACATCCTTGCCTCCCTTACATCCA 193
Db 5587 CGCCCTCTGCTAAAGCCGAGGACCCCCAACATCCTTGCCTCCCTTACATCCA 5646

QY 194 TGAGGCC 200

Db 5547 TCAGAC 553
; ORGANISM: Human
; US-10-027-632-166826
; Query Match 17.3%; score 37.4; DB 13; Length 765;
; Best Local Similarity 55.9%; Pred. No. 0.036; Gaps 0;
; Matches 71; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 810
; LENGTH: 662
; TYPE: DNA
; FEATURE: SITE
; NAME/KEY: SITE
; LOCATION: (321)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-764-891-810
; QUERY MATCH 24.7%; Score 53.4; DB 11; Length 662;
; Best Local Similarity 63.8%; Pred. No. 3.5e-07;
; Matches 81; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
; QY 74 TCTCGAGCAGGCCAAGCTCAACGCCAACACTGACAAAGGTGGGCTGAACGTA 133
; Db 28 TCTCCAGACAGACGACTACACCGTATGGCACTTCTCTAGGAGGGATAAGAGGA 87
; QY 134 CGCCCTGGCTAAGCGGACGTTACCCCAACACATCTTGCTCCCTTCCACTCCA 193
; Db 88 CCGCTCTAAACCTGACGAGCCAAAGCCTTCCTTGTGTCACATCCA 147
; QY 194 TGAGCC 200
; Db 148 TCAGACC 154
; RESULT 12
; US-10-027-632-166826/c
; Sequence 166826, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 100827129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32570
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1971
; TYPE: DNA
; ORGANISM: Aequorea victoria
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (0)...(1968)
; US-09-554-000-7
; QUERY MATCH 16.4%; Score 35.4; DB 10; Length 1971;
; Best Local Similarity 61.3%; Pred. No. 0.17; Gaps 0;
; Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
; QY 2 CGCGCCGCCCGAGGGACTCATCCAGGACGCTCCAGCACTGCC 61
; Db 112 CGCGTCCAGTCGACAGGATGGCACCCGGTGACACTCTCGCCCTGC 53
; QY 62 AGCCGTAATGCTGAGGACGCCAGCTCA 94
; Db 52 CGGGGGGGGCCAGGCCAGCA 20
; RESULT 14
; US-10-128-714-2578
; Sequence 2578, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wendi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskin, Alexey M
; APPLICANT: Lemieux, Sébastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714

